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Appeal Brief

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

First Named Inventor	:	Yumin Tao
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Title	:	Cell Cycle Polynucleotides, Polypeptides and Uses Thereof
Group/Art Unit	:	1638
Examiner	:	Collins, Cynthia A.
Attorney Docket Number	:	1109A

Assistant Commissioner for Patents
Washington, D.C. 20231

APPEAL BRIEF

This brief is in furtherance of the Notice of Appeal filed in this case on December 18, 2002.

The fees required under § 1.17, and any required petition for extension of time for filing this brief, and fees therefor, are dealt with in the accompanying Transmittal of Appeal Brief.

This brief is transmitted in triplicate.

Real Party in Interest

The subject application is owned by Pioneer Hi-Bred International, Inc. of Des Moines, Iowa.

Related Appeals and Interferences

To the best of my knowledge there are no related appeals or interferences that will directly affect or be directly affected by, or have a bearing on, the Board of Appeals decision in the pending appeal.

Status of Claims

This is an appeal from the Final Rejection of claims 2-18, 23-25, 27-53, 64, 66-69 and 71-74. Claims 1, 19-21, 26 and 54-63 were cancelled without prejudice. Claims 22, 65, 70 and 75 are allowed. Claims are on appeal. The claims on appeal are set out in the attached Appendix.

Status of Amendments

No amendment was filed subsequent to the Final Rejection of the claims.

Summary of the Invention

The present claimed invention provides novel isolated *cyclin E* nucleic acids. Such nucleic acids code for Cyclin E proteins that are involved in regulating the cell cycle.

As part of a complex with CDK2, Cyclin E (CycE) protein is an integral component required for phosphorylation of retinoblastoma. The phosphorylation of Rb results in the release of E2F, which then activates transcription of numerous genes involved in DNA replication. Thus CycE plays a significant role in the transition from G1 to S phase of the cell cycle and is involved in such processes as endocycling and organ pattern development.

Cells transformed to modulate the level of polypeptides that stimulate the transition of G1 to S phase will increase transformation frequencies compared to non-transformed plants. The transformation can be transient or stable, thus DNA, RNA, or proteins can be introduced into the cells. (Page 8, line 30 to page 9, line 19; Example 4 page 47, line 22 to page 48 line2 and Example 5 page 52; Example 8 page 58, line 10 to page 59, line 21 of the present application).

CycE can also be used to provide a differential growth advantage. CycE gene expression using tissue-specific or cell-specific promoters stimulates cell cycle progression in the expressing tissues or cells. For example, using a seed-specific promoter will stimulate the cell division rate and result in increased seed biomass.

Alternatively, driving CycE expression with a strongly-expressed, early, tassel-specific promoter will enhance development of this entire reproductive structure.

Expression of CycE genes in other cell types and/or at different stages of development will similarly stimulate cell division rates. Similar to results observed in Arabidopsis (Doerner et al., 1996), root-specific or root-preferred expression of CycE will result in larger roots and faster growth (i.e. more biomass accumulation). (Example 7 page 57 line 28 to page 58, line 8 of the present application)

Issues

1. Whether Claims 2-18, 23-25, 27-53, 64, 66-69 and 71-74 meet the written description requirement of 35 USC §112, first paragraph.

2. Whether Claims 2-18, 23-25, 27-53, 64, 66-69 and 71-74 meet the enablement requirement of 35 USC §112, first paragraph.

3. Whether Claims 16-18 meet the utility requirement under 35 USC § 101.

Grouping of the Claims

The claims do not stand or fall together. The patentability of the claims will be argued separately.

Arguments

Issue 1

1. Whether Claims 2-18, 23-25, 27-53, 64, 66-69 and 71-74 meet the written description requirement of 35 USC §112, first paragraph.

Claims 2-18, 23-25, 27-53, 64, 66-69 and 71-74 stand rejected over 35 USC §112, first paragraph as not meeting the written description requirement.

The Examiner maintains that the disclosure of one *CycE* nucleotide sequence encoding a functional CycE polypeptide is not sufficient to describe *CycE* polynucleotide sequences having 80% sequence identity to SEQ ID NO: 1 that also encode functional CycE polypeptides. The Examiner also maintains that procedures for making sequence variants that retain cyclin E activity are not conventional in the art. The Examiner further maintains that the specification does not disclose how the structure of the claimed invention is correlated with Cyclin E activity. (Office Action mailed February 25, 2002)

In the most recent Office Action, the Examiner states that an adequate written description of a claimed genus requires a description of both a structure and a function that is correlated with it. The Examiner also states that the rejected claims are not limited to the isolated nucleic acid of SEQ ID NO:1, or to isolated nucleic acids encoding a functional cyclin E protein. (Office Action mailed September 20, 2002).

The rejection is believed improper for the following reasons.

Based on current case law and USPTO Guidelines, it is submitted that the necessary written description requirements are met for the above-identified claims.

In *Amgen v. Chugai* The Federal Circuit held that "Conception does not occur unless **one has a mental picture of the structure of the chemical, or is able to define it by its method of preparation, its physical or chemical properties, or whatever characteristics sufficiently distinguish it**" *Amgen v. Chugai Pharmaceutical Co. Ltd.,* 18 USPQ1016, 1021 (Fed. Cir. 1991). See also *Ex parte Maizel*, 27 USPQ2d 1662, 1669 (B.P.A.I. 1992), citing Amgen v. Chugai, 927 F.2d 1200, 1206 (Fed. Cir. 1991).

Claims 64(b), 66 and 71 require an isolated nucleic acid comprising a polynucleotide having at least 80 % identity to SEQ ID NO: 1. The claims also require that the isolated nucleic acid is capable of modulating the level of Cyclin E protein. Conserved regions required for Cyclin E protein activity are defined in the present specification. The method of preparation of the claimed nucleic acids and

their physical or chemical properties are disclosed in the present application and are described in detail below.

In *University of California v. Eli Lilly and Co.* the Federal Circuit held that "description of a genus of cDNAs may be achieved by means of a recitation of a representative number of cDNAs, defined by nucleotide sequence, falling within the scope of the genus **or of a recitation of structural features common to the members of the genus, which features constitute a substantial portion of the genus**", *University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398, 1406 (Fed. Cir. 1997).

As noted above Claims 64(b), 66 and 71 provide the necessary structural features by requiring that the polynucleotides have at least 80% identity to SEQ ID NO: 1. Thus the claims recite structural features common to the members of the genus, which features constitute a substantial portion of the genus. The claims therefore meet the criteria set out in the *Lilly* case described above.

Claims 64(b), 66 and 71 also require the polynucleotide is capable of modulating the level of Cyclin E protein in a cell. Thus, the claims require a particular function. Nucleic acids that do not meet the function fall outside of the claim. Cyclin E protein is defined to meet certain structural and functional criteria as disclosed in the present application and discussed in detail below.

The Examiner states that the specification does not disclose a representative number of DNAs and that the mere recitation of sequences having varying degrees of sequence identity to SEQ ID NO: 1 does not meet the written description requirement. The Examiner further states that procedures for making sequence variants of cyclin E are not conventional in the art. (Page 3 of the Office Action mailed February 25, 2002)

The rejection is believed improper for the following reasons.

Under Example 9 of the Synopsis of Application of Written Description Guidelines (available at www.uspto.gov/web/menu/written.pdf, page 35), a claim to an isolated nucleic acid that hybridizes under highly stringent conditions to a

sequence is adequately described. Only one sequence is disclosed. However, the genus is adequately described because the highly stringent hybridization conditions set forth yield structurally similar DNAs. Therefore, an adequate number of representatives of the species is disclosed. In the present case, the claims are not to sequences capable of hybridizing under stringent conditions but to % identity, which strongly correlates with hybridization.

The USPTO addressed the "representative number" requirement in the Written Description Guidelines.

> A representative number of species means that the species which are adequately described are representative of the entire genus. Thus, when there is substantial variation within the genus, one must describe a sufficient variety of species to reflect the variation within the genus. On the other hand, **there may be situations where one species adequately supports a genus**. What constitutes a "representative number" is an inverse function of the skill and knowledge in the art. Satisfactory disclosure of a "representative number" **depends on whether one of skill in the art would recognize that the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed**. For inventions in an unpredictable art, adequate written description of a genus which embraces widely variant species cannot be achieved by disclosing only one species within the genus. **Description of a representative number of species does not require the description to be of such specificity that it would provide individual support for each species that the genus embraces.**

It is noted that the USPTO Written Description Guidelines provide that there may be situations where one species adequately supports a genus.

The Guidelines further state that satisfactory disclosure of a "representative number" depends on whether one of skill in the art would recognize that the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed. The Guidelines indicate that for some biomolecules, examples of identifying characteristics include a sequence, a structure, binding affinity, binding specificity, molecular weight and length.

The definition of CycE polynucleotide given in the present application is "a polynucleotide that encodes a polypeptide that i) binds to Cdk2 and Rb proteins, ii) contains a cyclin box (Jeffrey et al. 1995, Nature 367:313-320P, and iii) contains the conserved motif TTPXS near the carboxy-terminus". Claims 64(b), 66 and 71 also require at least 80% identity to SEQ ID NO:1. Thus CycE polynucleotides are well defined by structure and function. (See page 6, lines 3-6 of the present application) The claims require a polynucleotide capable of modulating the level of Cyclin E protein.

Therefore, one of skill in the art would recognize that the applicant was in possession of the necessary common attributes or features of the elements possessed by the members of the genus in view of the species disclosed.

Since the present claims require 80% identity to SEQ ID NO: 1, the claims do not read on "widely variant species" and therefore do not require a laundry list of potential sequences. Also one of skill in the art can readily determine if the criteria required by the claims is met.

Therefore, the present application provides more than adequate written description of CycE polynucleotides to show that the Applicant had possession of the invention at the time of filing.

The following discussion outlines the disclosure of the present application relating to obtaining acceptable variants.

The present application discloses that one can obtain homologous sequences from a plant by using primers based on the disclosed sequences. SEQ ID NOS: 3-6 describe specific primers that can be used in identifying maize homologues. See page 14, line 28 to page 15, line 2 and Example 1 pages page 44, line 29 to page 46, line 16 of the present application.

Obtaining silent variants and their use to detect allelic variants is disclosed on page 15, lines 3-9 of the present application.

Variants obtained by mutagenesis are disclosed on page 15, lines 10-16 of the present application.

Conservatively modified variants are disclosed on page 15, lines 17-24 of the present application.

Variants disclosed by gene shuffling are disclosed on page 15, lines 25-28 of the present application.

Variants obtained by codon optimization are disclosed on page 16, lines 5-21. Information on constructing nucleic acid libraries for obtaining variants is disclosed on page 18, lines 1-28 of the present application.

Hybridization conditions for obtaining variants are disclosed on page 18, line 29 to page 19, line 29 of the present application.

PCR amplification techniques for obtaining variants are described on page 19, line 30 to page 21, line 7 of the present application.

The Applicant has disclosed many methods for obtaining variants in the present application. The methods are well known in the art. It is respectfully submitted that disclosing additional *CycE* polynucleotide sequences would be of negligible value for determining how to vary SEQ ID NO: 1 to obtain a nucleic acid that encodes an active CycE protein.

Applicant would not receive the full benefit of his invention if others can avoid the claims by minor variations of the sequence disclosed in the present application. Such easy copying does not "promote the progress of science". Companies invest in technology when it can be protected. Lack of protection for technology does not benefit the inventor or the country.

Amended claim 2 limits the source of the isolated CycE polynucleotide to a monocot. Using the techniques described above and disclosed in detail in the present application, one skilled in the art can readily obtain a variant of SEQ ID NO: 1 from a monocot library.

Amended claim 3 further defines the source of the isolated CycE polynucleotide as maize. Using the primers, hybridization conditions and methods for developing libraries described above and disclosed in detail in the present

application, one skilled in the art can readily obtain a variant of SEQ ID NO: 1 from a monocot library.

Amended claim 4 defines the source of the isolated CycE polynucleotide as a dicot. Using the primers, hybridization conditions and methods for developing libraries described above and disclosed in detail in the present application, one skilled in the art can readily obtain a variant of SEQ ID NO: 1 from a dicot library.

Amended claim 5 defines the source of the isolated CycE polynucleotide as a soybean. Using the primers, hybridization conditions and methods for developing libraries described above and disclosed in detail in the present application, one skilled in the art can readily obtain a variant of SEQ ID NO: 1 from a soybean library.

Amended claim 6 requires the isolated CycE polynucleotide has the sequence of SEQ ID NO:1. The scope of claim 6 is comparable to allowed claim 70 and presumed allowable if base claim 64 is allowed.

Amended claim 7 requires that the polynucleotide is DNA.

Amended claim 8 requires that the polynucleotide is RNA.

Amended claim 9 requires that the isolated nucleic acid is adducted to a second nucleic acid sequence encoding a DNA-binding domain. The method is discussed on page 30, lines 15-22 and Example 3 page 47 of the present application.

Amended claim 10 provides for a vector comprising the nucleic acid. Examples of vector components are listed in the present application. See page 17, lines 3-12 to page 17, line 22. Vectors generally comprise expression cassettes or components described on page 21, line 25 to page 24, line 30. Expression cassettes generally include a promoter or regulatory region and a coding region for a gene of interest or for silencing a gene of interest.

Amended claim 11 provides for an expression cassette comprising the claimed nucleic acid operably linked in antisense orientation to a promoter. Antisense and other methods of gene silencing are discussed on page 24, line 26 to page 25, line 14 of the present application.

Claim 12 provides for an expression cassette where the isolated nucleic acid is operably linked in sense orientation to the promoter.

Amended 13 claims a non-human host cell. Host cells are discussed on page 27, line 28 to page 28, line 9.

Claim 14 requires the host cell is a prokaryote or a plant cell. As noted above host cells are described on page 27, line 28 to pate 28 line 9.

Claim 15 requires the host cell is a specific plant cell. The specific plant cells are described on page 31, lines 14-16 and page 42, lines 13-18 of the present application.

Claim 16 calls for a transgenic plant comprising at least one expression cassette of claim 11. Methods for transforming and regenerating transformed plants are described on page 35, line 16 to page 42, line 24 of the present application and Examples 4-8.

Claim 17 further defines specific plants. The specific plants are described on page 31, lines 14-16 and page 42, lines 13-18 of the present application.

Amended claim 18 calls for seed comprising the expression cassette of claim 11.

Amended claim 23 recites a method of modulating the level of CycE protein in a cell. The method comprises transforming a cell with the expression cassette of claim 11. Expression cassettes and methods of transformation and regeneration are described above.

Claim 24 requires that the level of CycE is increased. Methods of increasing the level of CycE are discussed above with regard to sense expression.

Claim 25 requires that the level of CycE is decreased. Methods of decreasing the level of CycE are discussed above with regard to antisense expression.

Claims 27-53 define various results and advantages of practicing the methods of claim 23-25 and are considered independently patentable.

The Examiner's rejection of amended claim 64 and claims 66 and 71 is discussed above with regard to claiming a sequence with 80% identity to SEQ ID

NO:1. The Examiner has indicated allowable subject matter for sections (a), (c) and (d) of amended claim 64.

Claims 67 and 72 require at least 85% identity to SEQ ID NO:1. As discussed in detail above, variants of SEQ ID NO: 1 having the required identity and that encode the CycE polypeptide.

Claims 68 and 73 require at least 90% identity to SEQ ID NO: 1. Such sequences can be identified by one skilled in the art by using the methods summarized above and described in detail in the present application.

Claims 69 and 74 require at least 95% identity to SEQ ID NO: 1. Such sequences can be identified by one skilled in the art by using the methods summarized above and described in detail in the present application.

In conclusion, the present application clearly defines the claimed CycE polynucleotides, how to identify them and how to obtain them. Therefore, it is respectfully submitted that the present application provides sufficient written description to support the current claims. One skilled in the art would understand that the inventors had possession of the invention at the time of filing.

Issue 2

2. Whether Claims 2-18, 23-25, 27-53, 64, 66-69 and 71-74 meet the enablement requirement of 35 USC §112, first paragraph.

Claims 2-18, 23-25, 27-53, 64, 66-69 and 71-74 stand rejected under 35 USC §112, first paragraph for scope of enablement. The Examiner maintains that the scope of the invention is not enabled.

The Examiner states that the specification does not reasonably provide enablement for a CycE polynucleotide having at least 80% identity to the entire coding region of SEQ ID NO: 1 and complementary nucleotides thereof. The Examiner concludes that the scope of the invention is not enabled because of the unpredictability of determining the function of isolated nucleic acids homologous to

SEQ ID NO: 1, and because of the unpredictability of altering the phenotype of a plant by transforming it with isolated nucleic acids homologous to SEQ ID NO: 1. (Office Action mailed September 17, 2001).

The Examiner also maintains that the disclosure of methods to identify compositions and assays to determine their functionality does not enable the invention in the absence of the disclosure of the structural features of the claimed sequences that are critical to the claimed functions. (Office Action mailed February 25, 2002)

The Examiner maintains that the disclosure of methods for finding functional variants does not provide sufficient guidance for one skilled in the art to determine, without undue experimentation, which isolated nucleic acids encode a functional protein as the specification does not disclose such a nucleic acid. The Examiner maintains that the undue experimentation lies in the process of selecting from among the numerous isolated nucleic acids that could be used to practice the claimed invention, as the claimed invention is not limited to isolated nucleic acids encoding functional cyclin E proteins, but is directed also to methods whose results are highly unpredictable. (Office Action mailed September 20, 2002).

As detailed above with regard to written description, the specification provides not only the full-length polynucleotide sequences of the present invention, but also guidance on modifications and variants as well as methods to identify compositions. Although assaying will be required to identify candidates, this does not mean the invention is not enabled. For example, using only the degeneracy of the genetic code, one could produce a polynucleotide of 80% sequence identity to the sequences claimed without changing the amino acid sequence of the encoded polypeptide.

With regard to structural features of the claimed sequences, as noted above the claims require a polynucleotide capable of modulating the level of a Cyclin E protein. The Cyclin E protein is defined in the present specification as comprising certain conserved regions. These conserved regions are a cyclin box and the

conserved motif TTPXS near the carboxy-terminus. Functionally the CycE protein binds to Cdk2 and Rb proteins.

Thus, it is respectfully submitted that the specification describes the invention in sufficient detail to reasonably convey the scope of the invention. The testing to determine functionality is routine.

In re Wands, 858 F.2d 731, 8 USPQ 2d 1400 (Fed. Cir. 1988) lists eight considerations for determining whether or not undue experimentation would be necessary to practice an invention. These factors are: the quantity of experimentation necessary, the amount of direction or guidance presented, the presence or absence of working examples of the invention, the nature of the invention, the state of the prior art, the relative skill of those in the art, the predictability or unpredictability of the art, and the breadth of the claims.

When determining the quantity of experimentation necessary, the focus is not on the amount of experimentation necessary to practice the entire genus, but the amount of experimentation required to practice any particular member. This concept is the central holding of *In re Wands* where the claims read on the use of any IgM antibody that possessed a particular binding affinity.

The *Wands* court recognized that it would require an infinite amount of experimentation to obtain every single possible IgM antibody that could be generated with the specified affinity. Accordingly, the court focused on the amount of experimentation necessary to practice any particular IgM antibody with the recited binding affinity and not the amount of experimentation required to practice the entire genus.

The question then becomes how much experimentation is required to create the present claimed invention. Applicants submit that no more than routine experimentation is required to practice any particular sequence. This may be accomplished by the methods disclosed in the present application and within the technical, scientific, skill in the art.

This focus is further supported by the multitude of chemical patents that have issued with generic claims reading on tens to hundreds of thousands of individual members. Patent law with regard to chemical patents is well established and should provide a proper guideline for biotech patents. The court in *Amgen* stated that DNA was a chemical compound albeit a complex one, and that in light of this classification it would be appropriate to apply chemical case law precedent to cases involving the patentability of DNA sequences.

Applicants assert the present invention is disclosed in a way that one skilled in the art will be able to practice it without an undue amount of experimentation. Applicants submit that they have fully described the present invention as claimed by teaching both how to make and how to use the invention in a manner commensurate in scope with the claims.

The USPTO carries the initial burden to establish a reasonable basis for questioning the enablement provided for the claimed invention. As stated in *In re Wright*, 99, F.2d 1557, 27 USPQ2d 1510 (Fed. Cir. 1993); MPEP § 2164.04, the enablement requirement is satisfied if the specification describes any method for making and using the claimed invention that bears a "reasonable correlation" to the entire scope of the claims. Applicants submit that this has been accomplished in the present application.

Sequences obtained with less than 100% identity could easily be tested for activity using the methods outlined in the present application as described in detail above. "That one skilled in the art must perform some preliminary tests or experiments before he can make or use the invention does not invalidate the patent" on the basis of section 112. *Atlas Powder Co. v. E. I. Du Pont De Nemours & Co.*, 750 F.2d 1569, 1576 (Fed. Cir. 1984). Thus, polynucleotides having less than 100% identity, which also encode for functional CycE polypeptides, can easily be found without undue experimentation.

It is submitted that additional specific sequences are not necessary to provide enablement for claims requiring a sequence having at least 80% sequence identity

to SEQ ID NO 1. As discussed in detail above, the present application provides general methods for obtaining functional sequences that have at least 80% sequence identity to SEQ ID NO 1.

Further many patents containing open-ended R groups are issued in the chemical and pharmacological disciplines that result in innumerable possible structures. The present specification and claims certainly provide at least as much direction as to the structure of the claimed nucleic acid. The law in the chemical and pharmacological disciplines is well established and it is appropriate for the Patent Office to apply consistent rulings to biotech cases. As noted above, the court in *Amgen* stated that DNA was a chemical compound, and that in light of this classification it would be appropriate to apply chemical case law precedent to cases involving the patentability of DNA sequences.

The arguments with regard to specific dependent claims relating to the written description rejection, apply equally well for enablement and are incorporated herein by reference for the sake of brevity.

Issue 3

3. Whether Claims 16-18 meet the utility requirement under 35 USC § 101.

Claims 16-18 stand rejected under 35 USC § 101 as not being supported by a specific and substantial utility.

The Examiner states that since nontransformed plants already possess endogenous cyclin E genes, the claimed invention is not supported by a specific and substantial utility in the absence of evidence that the claimed transgenic plants and see have some specific and substantial utility relative to nontransformed plants.

There is clear evidence in the literature as described in the present application that over expression of CycE produces altered affects on transformed cells. In fact, overexpression of any gene generally alters the phenotype of a plant.

The following information is provided in the present application.

Similar to Cyclin-D (another G1-S phase stimulating protein) CycE genes from heterologous species have been found to complement Saccharomyces cerevisiae cells lacking the G1 cyclin function required for progression through START. CycE overexpression has been found to stimulate S-phase in various cell types in both Drosophila and mammalian cells (Ohtsubo, M., Roberts, J.M., 1993, Science 259:1908-1912; Wimmels, A., Lucibello, F.C., Sewing, A., Adolf, S, Muller, R., 994, Oncogene 9:995-997; Resnitzky, D.M.G., Bujard, H., Reed, S.I., 1994, Mol Cell Biol. 14:1669-1679; Ohtsubo, M., Theadoras, A.M., Schumacher, J., Roberts, J.M., Pagano, M., 1995, Mol Cell Biol. 15:2612-2624. Evidence across a variety of fauna including Homo sapiens, Drosophila melanogaster, Xenopus laevis, zebrafish and mice suggests that the role of CycE is similar across these genera; activity of this protein promotes cell cycle entry into S-phase and is involved in such processes as endocycling and organ pattern development. (See page 9, lines 3-15 of the present application)

Further, published application WO 00/17364 discloses increased transformation results for a related cyclin, Cyclin D.

Therefore, a specific and substantial utility is provided for the claimed Cyclin E polynucleotides.

In view of the foregoing remarks, reversal of the outstanding rejections and allowance of the pending claims is respectfully requested.

Respectfully submitted,

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APPENDIX OF CLAIMS

The text of the claims in the appeal are:

2. The isolated nucleic acid of claim 64, wherein the polynucleotide is from a monocot.

3. The isolated nucleic acid of claim 2, wherein the polynucleotide is from maize.

4. The isolated nucleic acid of claim 64, wherein the polynucleotide is from a dicot.

5. The isolated nucleic acid of claim 4, wherein the polynucleotide is from soybean.

6. The isolated nucleic acid of claim 64, wherein the polynucleotide has the sequence of SEQ ID NO: 1.

7. The isolated nucleic acid of claim 64, wherein the polynucleotide is DNA.

8. The isolated nucleic acid of claim 64, wherein the polynucleotide is RNA.

9. The isolated nucleic acid of claim 64 adducted to a second nucleic acid sequence encoding a DNA-binding domain.

10. A vector comprising at least one nucleic acid of claim 64.

11. A recombinant expression cassette comprising a nucleic acid of claim 64 operably linked to a promoter in sense or antisense orientation.

12. The recombinant expression cassette of claim 11, wherein the nucleic acid is operably linked in sense orientation to the promoter.

13. A non-human host cell containing the recombinant expression cassette of claim 11.

14. The host cell of claim 13 that is a procaryote or a plant cell.

15. The host cell of claim 14 that is a corn, soybean, sorghum, sunflower, safflower, wheat, rice, alfalfa or oil-seed *Brassica* cell.

16. A transgenic plant comprising at least one expression cassette of claim 11.

17. The plant of claim 16 that is corn, soybean, sorghum, sunflower, safflower, wheat, rice, alfalfa or oil-seed *Brassica*.

18. A seed comprising the expression cassette of claim 11.

23. A method of modulating the level of CycE protein in a cell, comprising:
    (a) transforming a plant cell with a recombinant expression cassette of claim 11;
    (b) growing the plant cell under cell-growing conditions for a time sufficient to induce expression of the polynucleotide sufficient to modulate CycE protein in the cell.

24. The method of claim 23, wherein CycE protein is increased.

25. The method of claim 23, wherein CycE protein is decreased.

27. The method of claim 23, wherein the CycE protein is present in an amount sufficient to alter cell division.

28. The method of claim 23, wherein the CycE protein is present in an amount sufficient to increase the number of dividing cells.

29. The method of claim 23, wherein the CycE protein is present in an amount sufficient to improve transformation frequencies.

30. The method of claim 23, wherein the CycE protein is present in an amount sufficient to alter cell growth.

31. The method of claim 23, wherein the CycE protein is present in an amount sufficient to provide a positive growth advantage for the cell.

32. The method of claim 23, wherein the CycE protein is present in an amount sufficient to increase the growth rate.

33. The method of claim 23, wherein the cell is a plant cell and the plant cell is grown under conditions appropriate for regenerating a plant capable of expressing CycE protein.

34. The method of claim 33, wherein the plant cell is from corn, soybean, wheat, rice, alfalfa, sunflower, safflower, or canola.

35. The method of claim 33, wherein the CycE protein is present in an amount sufficient to increase crop yield.

36. The method of claim 33, wherein the CycE protein is present in an amount sufficient to alter plant height or size.

37. The method of claim 33, wherein the CycE protein is present in an amount sufficient to enhance or inhibit organ growth.

38. The method of claim 37, wherein the organ is a seed, root, shoot, ear, tassel, stalk, pollen, or stamen.

39. The method of claim 38, wherein the level of CycE protein is modulated to produce organ ablation.

40. The method of claim 38, wherein the level of CycE protein is modulated to produce parthenocarpic fruits.

41. The method of claim 38, wherein the level of CycE protein is modulated to produce male sterile plants.

42. The method of claim 33, wherein the CycE protein is present in an amount sufficient to enhance embryogenic response.

43. The method of claim 33, wherein the CycE protein is present in an amount sufficient to increase callus induction.

44. The method of claim 33, wherein the level of CycE protein is modulated to provide for positive selection.

45. The method of claim 33, wherein the level of CycE protein is modulated to increase plant regeneration.

46. The method of claim 23, wherein the level of CycE protein is modulated to alter the percent of time that the cells are arrested in G1 or G0 phase.

47. The method of claim 23, wherein the level of CycE protein is modulated to alter the amount of time the cell spends in a particular cell cycle.

48. The method of claim 23, wherein the level of CycE protein is modulated to improve the response of the cells to environmental stress including dehydration, heat, or cold.

49. The method of claim 33, wherein the level of CycE protein is modulated to increase the number of pods per plant.

50. The method of claim 33, wherein the level of CycE protein is modulated to increase the number of seeds per pod or ear.

51. The method of claim 33, wherein the level of CycE protein is modulated to alter the lag time in seed development.

52. The method of claim 33, wherein the level of CycE protein is modulated to provide hormone independent cell growth.

53. The method of claim 23, wherein the level of CycE protein is modulated to increase the growth rate of cells in bioreactors.

64. An isolated nucleic acid capable of modulating the level of Cyclin E protein, wherein the nucleic acid comprises a member selected from the group consisting of:

(a) a polynucleotide that encodes a polypeptide of SEQ ID NO: 2;

(b) a plant Cyclin E polynucleotide having at least 80% identity to the entire coding region of SEQ ID NO: 1, wherein the % identity is determined by GCG/bestfit GAP 10 program using a gap creation penalty of 50 and a gap extension penalty of 3;

(c) a polynucleotide having the sequence set forth in SEQ ID NO: 1; and

(d) a polynucleotide fully complementary to a polynucleotide of (a) through (c).

66. An isolated nucleic acid capable of modulating the level of Cyclin E protein in a cell, wherein the nucleic acid comprises a polynucleotide having at least 80% identity to the entire coding region of SEQ ID NO: 1, wherein the % identity is determined by GCG/bestfit GAP 10 program using default parameters.

67. The isolated nucleic acid of claim 66, wherein the polynucleotide has at least 85% identity.

68. The isolated nucleic acid of claim 67, wherein the polynucleotide has at least 90% identity.

69. The isolated nucleic acid of claim 68, wherein the polynucleotide has at least 95% identity.

71. An isolated nucleic acid capable of modulating the level of Cyclin E protein in a cell, wherein the nucleic acid comprises a polynucleotide fully complementary to at least 80% of the entire coding region of SEQ ID NO: 1, wherein the % identity is determined by GCG/bestfit GAP 10 program using default parameters.

72. The isolated nucleic acid of claim 71, wherein the polynucleotide has at least 85% identity.

73. The isolated nucleic acid of claim 72, wherein the polynucleotide has at least 90% identity.

74. The isolated nucleic acid of claim 73, wherein the polynucleotide has at least 95% identity.